

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/898,165

DATE: 07/24/2001
TIME: 10:44:59

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\07242001\I898165.raw

ENTERED

4 <110> APPLICANT: Daniel H. Cohn
5 Muhammad Faiyaz ul Haque
6 Lily M. King
7 Deborah Krakow
9 <120> TITLE OF INVENTION: 3-PHOSPHOADENOSINE-5-PHOSPHOSULFATE
10 (PAPS) SYNTHETASE PROTEINS AND METHODS FOR TREATING
11 OSTEOARTHRITIC DISORDERS
13 <130> FILE REFERENCE: 18810-81552
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/898,165
16 <141> CURRENT FILING DATE: 2001-07-02
18 <150> PRIOR APPLICATION NUMBER: 09/399,212
19 <151> PRIOR FILING DATE: 1999-09-17
21 <160> NUMBER OF SEQ ID NOS: 28
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2014
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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32 ctccgcgcgca gccagccagc atgtcgggga tcaagaagca aaagacggag aaccagcaga 120
33 aatccaccaa tgtagtctat caggcccacc atgtgagcag gaataagaga gggcaagtgg 180
34 ttggaacaag ggggtgggttc cgaggatgta ccgtgtggct aacagggtctc tctgggtgctg 240
35 gaaaaacaac gataagtttt gccctggagg agtaccttgt ctcccatgcc atcccttgtt 300
36 actccctgga tggggacaat gtccgtcatg gccttaacag aaatctcgga ttctctcctg 360
37 gggacagaga ggaaaatata cgcgcggattg ctgaggtggc taagctgttt gctgatgctg 420
38 gtctgggtctg cattaccagc tttattttctc cattcgcaaa ggatcgtgag aatgcccgcg 480
39 aaatacatga atcagcaggg ctgccattct ttgaaatatt tgtagatgca cctctaaata 540
40 tttgtgaaag cagagacgta aaaggcctct ataaaagggc cagagctggg gagattaaag 600
41 gatttacagg tattgattct gattatgaga aacctgaaac tcctgagcgt gtgcttaaaa 660
42 ccaatttgtc cacagttagt gactgtgtcc accaggtagt ggaacttctg caagagcaga 720
43 acattgtacc ctatactata atcaaagata tccacgaact ctttgtgccg gaaaacaaac 780
44 ttgaccacgt ccgagctgag gctgaaactc tcccttcatt atcaattact aagctggatc 840
45 tccagtgggt ccaggttttg agcgaaggct gggccactcc cctcaaagg ttcagtgcgg 900
46 agaaggagta cttacagggt atgcactttg acaccctgct agatgatggc gtgatcaaca 960
47 tgagcatccc cattgtactg cccgtctctg cagaggataa gacacggctg gaagggtgca 1020
48 gcaagtttgt cctggcacat ggtggacgga gggtagctat cttacgagac gctgaattct 1080
49 atgaacacag aaaagaggaa cgctgttccc gtgtttgggg gacaacatgt acaaaacacc 1140
50 cccatatcaa aatggtgatg gaaagtgggg actggctggg tgggtggagac cttcaggtgc 1200
51 tggagaaaaa aagatggaat gatgggctgg accaataccg tctgacacct ctggagctca 1260
52 aacagaaatg taaagaaatg aatgctgatg cgggtgtttg attccagttg cgcaatcctg 1320
53 tccacaatgg ccatgccctg ttgatgcagg acacctgccg caggctccta gagaggggct 1380
54 acaagcaccg ggtcctccta ctacaccctc tgggcgggct gaccaaggat gacgatgtgc 1440
55 ctctagactg gcggatgaag cagcacgcgg ctgtgctcga ggaaggggtc ctggatccca 1500
56 agtcaaccat tgttgccatc ttccgtctc ccatgttata tgctggcccc acagaggtcc 1560
57 agtggcactg caggtcccg atgattgcgg gtgccaat tctacattgtg gggagggacc 1620
58 ctgcaggaat gccccatcct gaaaccaaga aggatctgta tgaaccact catgggggca 1680

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59 aggtcttgag catggccctt ggcctcacct ctgtggaaat cattccattc cgagtggctg 1740
60 cctacaacaa agccaaaaaa gccatggact tctatgatcc agcaaggcac aatgagtttg 1800
61 acttcatctc aggaactcga atgaggaagc tcgcccggga aggagagaat cccccagatg 1860
62 gcttcatggc ccccaaagca tggaaaggtc tgacagatta ttacaggtcc ctggagaaga 1920
63 actaagcctt tgggtccaga gtttctttct gaagtgtctt ttgattacct tttctatatt 1980
64 tatgattaga tgctttgtat taaattgctt ctca 2014

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66 <210> SEQ ID NO: 2

67 <211> LENGTH: 2000

68 <212> TYPE: DNA

69 <213> ORGANISM: Mus musculus

71 <400> SEQUENCE: 2

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72 gtattctcaa catcagatat catgtcttgg aggaagttac ctaaactctg aagaattatc 60
73 atgtctgcaa atttcaaaat gaaccataaa agagaccagc aaaaatccac caatgtgggtc 120
74 taccaggccc atcatgtgag caggaacaag agaggacaag tggttggaac caggggagga 180
75 ttccgaggat gtaccgtgtg gctaacaggt ctctctggtg ctgggaaaac aaccataagc 240
76 tttgcttttg aagagtacct tgtatctcac gccatcccat gttactccct ggatggggac 300
77 aatgtccgtc atggccttaa taagaacctg ggattctctg ccggggaccg agaagagaat 360
78 atccgccgga tcgcgagggt ggccaagctc tttgccgacg ccggcctggt ttgcatcacc 420
79 agcttttatct ctcccttttg aaaggatcgt gagaatgccg gaaaaatcca cgaatcagca 480
80 ggactcccggt tctttgagat cttttagatg gcgcctttaa atatctgtga aagccgagac 540
81 gtaaaaggac tctacaaacg agcccagaca ggagagatta aagggtttac aggcactcat 600
82 tctgactatg agaaacctga aactccagag tgtgtgctga agaccaactt gtcttcagta 660
83 agcgactgtg tgcaacaggt ggtggaactt ttgcaggagc agaacattgt accccacacc 720
84 accatcaaag gcatccacga actctttgtg ccagaaaaca aagtcgatca aatccgagct 780
85 gaggcagaga ctctcccatc actaccaatt accaagctgg atctgcagtg ggtgcagatt 840
86 ctgagtgaag gctggggccac tcccctcaaa ggctttatgc gggagaagga atacttgcaa 900
87 actctacact tcgacactct actggacgat ggagtcatca acatgagtat tcccattgta 960
88 ttgcccgttt ctgcgatga caaggcacgg ctgcaagggt gcagcaaatt tgccttgatg 1020
89 tacgaagggt ggagggtcgc tctattacag gacctgaat tctatgagca taggaaagag 1080
90 gagcgttggt ctctgtgtgt gggaacagcc actgcaaagc acccccatat caaaatggtg 1140
91 atggaaagtg gggactggct tgttgggtga gacctacagg tgctagagag aataagggtg 1200
92 gacgatgggc tggaccaata ccgccttacg cctctggaac tcaaacagaa gtgtaaagac 1260
93 atgaatgctg atgccgtgtt tgcattccag ttgcgcaatc ctgtccacaa tggatcatgc 1320
94 ctccctgatg aggacacccg ccgcaggctc ctggagaggg gttacaagca cccagtcctc 1380
95 ctgctccacc ctcttggggg ctggaccaag gacgatgacg tacctctgga atggaggatg 1440
96 aaacagcatg cagctgtact ggaggaaagg gtccctggatc ccaagtcaac tattgttgcc 1500
97 atctttccat ctccatgttt atacgtgggt cccacagagg tccagtggca ttgcagatgc 1560
98 cggatgattg caggagccaa tttctacatt gtgggtaggg atcccgcagg aatgccccat 1620
99 cctgagacaa agaaagacct atatgaacct acccacggg gcaaggctct gagtatggcc 1680
100 cctggcctta cctctgtgga aataattccg ttccgagtgg ctgcctacaa taaaattaaa 1740
101 aaggccatgg acttttatga tccagcaagg cagcaggagt ttgacttcat ctcaggaact 1800
102 cgcattgaga agctcgcccc ggaaggagaa gatccccagc atggcttcat ggccccgaaa 1860
103 gcgtggaaag tgttgacaga ttactacagg tctctggaga agaccaacta ggtgctctct 1920
104 gctctggctt ctccctcaag tgcctctctg cgattttttt tttctatatt tgtgatttag 1980
105 ctgctctgta tccaattgca 2000

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107 <210> SEQ ID NO: 3

108 <211> LENGTH: 20

109 <212> TYPE: DNA

110 <213> ORGANISM: Homo sapiens

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112 <400> SEQUENCE: 3
113 tggaccaagg atgacgatgt                                20
115 <210> SEQ ID NO: 4
116 <211> LENGTH: 20
117 <212> TYPE: DNA
118 <213> ORGANISM: Homo sapiens
120 <400> SEQUENCE: 4
121 cggaaagatg gcaacaatgg                                20
123 <210> SEQ ID NO: 5
124 <211> LENGTH: 20
125 <212> TYPE: DNA
126 <213> ORGANISM: Homo sapiens
128 <400> SEQUENCE: 5
129 ctggtgctgg aaaaacaacg                                20
131 <210> SEQ ID NO: 6
132 <211> LENGTH: 22
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 6
137 tgcgaatgga gaaataaagc tg                                22
139 <210> SEQ ID NO: 7
140 <211> LENGTH: 615
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 7
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147 Asn Val Val Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln
148          20          25          30
149 Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr
150          35          40          45
151 Gly Leu Ser Gly Ala Gly Lys Thr Thr Ile Ser Phe Ala Leu Glu Glu
152          50          55          60
153 Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp Asn
154 65          70          75          80
155 Val Arg His Gly Leu Asn Arg Asn Leu Gly Phe Ser Pro Gly Asp Arg
156          85          90          95
157 Glu Glu Asn Ile Arg Arg Ile Ala Glu Val Ala Lys Leu Phe Ala Asp
158          100         105         110
159 Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys Asp
160          115         120         125
161 Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe Phe
162          130         135         140
163 Glu Ile Phe Val Asp Ala Pro Leu Asn Ile Cys Glu Ser Arg Asp Val
164 145          150         155         160
165 Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr
166          165         170         175
167 Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Arg Val Leu
168          180         185         190

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169 Lys Thr Asn Leu Ser Thr Val Ser Asp Cys Val His Gln Val Val Glu
170      195      200      205
171 Leu Leu Gln Glu Gln Asn Ile Val Pro Tyr Thr Ile Ile Lys Asp Ile
172      210      215      220
173 His Glu Leu Phe Val Pro Glu Asn Lys Leu Asp His Val Arg Ala Glu
174 225      230      235      240
175 Ala Glu Thr Leu Pro Ser Leu Ser Ile Thr Lys Leu Asp Leu Gln Trp
176      245      250      255
177 Val Gln Val Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe Met
178      260      265      270
179 Arg Glu Lys Glu Tyr Leu Gln Val Met His Phe Asp Thr Leu Leu Asp
180      275      280      285
181 Asp Gly Val Ile Asn Met Ser Ile Pro Ile Val Leu Pro Val Ser Ala
182      290      295      300
183 Glu Asp Lys Thr Arg Leu Glu Gly Cys Ser Lys Phe Val Leu Ala His
184 305      310      315      320
185 Gly Gly Arg Arg Val Ala Ile Leu Arg Asp Ala Glu Phe Tyr Glu His
186      325      330      335
187 Arg Lys Glu Glu Arg Cys Ser Arg Val Trp Gly Thr Thr Cys Thr Lys
188      340      345      350
189 His Pro His Ile Lys Met Val Met Glu Ser Gly Asp Trp Leu Val Gly
190      355      360      365
191 Gly Asp Leu Gln Val Leu Glu Lys Ile Arg Trp Asn Asp Gly Leu Asp
192      370      375      380
193 Gln Tyr Arg Leu Thr Pro Leu Glu Leu Lys Gln Lys Cys Lys Glu Met
194 385      390      395      400
195 Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn
196      405      410      415
197 Gly His Ala Leu Leu Met Gln Asp Thr Cys Arg Arg Leu Leu Glu Arg
198      420      425      430
199 Gly Tyr Lys His Pro Val Leu Leu Leu His Pro Leu Gly Gly Trp Thr
200      435      440      445
201 Lys Asp Asp Asp Val Pro Leu Asp Trp Arg Met Lys Gln His Ala Ala
202      450      455      460
203 Val Leu Glu Glu Gly Val Leu Asp Pro Lys Ser Thr Ile Val Ala Ile
204 465      470      475      480
205 Phe Pro Ser Pro Met Leu Tyr Ala Gly Pro Thr Glu Val Gln Trp His
206      485      490      495
207 Cys Arg Ser Arg Met Ile Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg
208      500      505      510
209 Asp Pro Ala Gly Met Pro His Pro Glu Thr Lys Lys Asp Leu Tyr Glu
210      515      520      525
211 Pro Thr His Gly Gly Lys Val Leu Ser Met Ala Pro Gly Leu Thr Ser
212      530      535      540
213 Val Glu Ile Ile Pro Phe Arg Val Ala Ala Tyr Asn Lys Ala Lys Lys
214 545      550      555      560
215 Ala Met Asp Phe Tyr Asp Pro Ala Arg His Asn Glu Phe Asp Phe Ile
216      565      570      575
217 Ser Gly Thr Arg Met Arg Lys Leu Ala Arg Glu Gly Glu Asn Pro Pro

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218          580          585          590
219 Asp Gly Phe Met Ala Pro Lys Ala Trp Lys Val Leu Thr Asp Tyr Tyr
220          595          600          605
221 Arg Ser Glu Met Asp Lys Asn
222    610          615
225 <210> SEQ ID NO: 8
226 <211> LENGTH: 617
227 <212> TYPE: PRT
228 <213> ORGANISM: Mus musculus
230 <400> SEQUENCE: 8
231 Met Ser Ala Asn Phe Lys Met Asn His Lys Arg Asp Gln Gln Lys Ser
232 1          5          10          15
233 Thr Asn Val Val Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly
234          20          25          30
235 Gln Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu
236    35          40          45
237 Thr Gly Leu Ser Gly Ala Gly Lys Thr Thr Ile Ser Phe Ala Leu Glu
238    50          55          60
239 Glu Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp
240 65          70          75          80
241 Asn Val Arg His Gly Leu Asn Lys Asn Leu Gly Phe Ser Ala Gly Asp
242          85          90          95
243 Arg Glu Glu Asn Ile Arg Arg Ile Ala Glu Val Ala Lys Leu Phe Ala
244          100          105          110
245 Asp Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys
246          115          120          125
247 Asp Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe
248          130          135          140
249 Phe Glu Ile Phe Val Asp Ala Pro Leu Asn Ile Cys Glu Ser Arg Asp
250 145          150          155          160
251 Val Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe
252          165          170          175
253 Thr Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Cys Val
254          180          185          190
255 Leu Lys Thr Asn Leu Ser Ser Val Ser Asp Cys Val Gln Gln Val Val
256          195          200          205
257 Glu Leu Leu Gln Glu Gln Asn Ile Val Pro His Thr Thr Ile Lys Gly
258          210          215          220
259 Ile His Glu Leu Phe Val Pro Glu Asn Lys Val Asp Gln Ile Arg Ala
260 225          230          235          240
261 Glu Ala Glu Thr Leu Pro Ser Leu Pro Ile Thr Lys Leu Asp Leu Gln
262          245          250          255
263 Trp Val Gln Ile Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe
264          260          265          270
265 Met Arg Glu Lys Glu Tyr Leu Gln Thr Leu His Phe Asp Thr Leu Leu
266          275          280          285
267 Asp Asp Gly Val Ile Asn Met Ser Ile Pro Ile Val Leu Pro Val Ser
268          290          295          300
269 Ala Asp Asp Lys Ala Arg Leu Glu Gly Cys Ser Lys Phe Ala Leu Met

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/898,165

DATE: 07/24/2001

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Input Set : A:\seqlist.txt

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number